



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Green et al.

Serial No. 09/837,751

Filed: April 18, 2001

For: METHOD OF MODIFYING THE
CONTENT OF COTTONSEED OIL

:

: Group Art Unit: 1651

: Examiner: Not yet assigned

:

#5

STATEMENT UNDER 37 C.F.R. §1.821-824

Commissioner for Patents
BOX MISSING PARTS
Washington, D.C. 20231

Sir:

The above-identified patent application contained sequences as defined in 37 C.F.R. §1.821(a). Accordingly, the specification included a paper copy of Sequence Listing as pages 1 - 25. In response to Notice to File Missing Parts of Nonprovisional Application filed herewith, that paper copy (pages 1 - 25) is being cancelled and a substitute paper (pages 1 - 30) is provided herewith. Applicants also submit a write-protected diskette copy of the replacement Sequence Listing in computer-readable form as required by 37 C.F.R. §1.821(e).

In compliance with 37 C.F.R. §1.821(f), the undersigned states that the content of the substitute paper copy and computer-readable copy of the Sequence Listing as enclosed herewith, are the same.

Respectfully submitted,

Donna M. Ferber
Reg. No. 33,878

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Attorney Docket No.: 45-00
bmk: November 1, 2001

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to the Commissioner for Patents, Washington, D.C., 20231

1 November 2001 B. Kroge
Date B. Kroge



#5

SEQUENCE LISTING

<110> Green, Allan
Singh, Surinder
Liu, Qing

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<140> 09/837,751

<141> 2001-04-18

<150> US 60/198,124

<151> 2000-04-18

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<170> PatentIn Ver. 2.0

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Pro	Ala	Asp	Phe	Leu	Pro	Asp	Pro	Asn	Ser	Asp	Gly	Phe	His	Glu	Gln	100	105	110	
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Ser	Ile	Ala	Ser	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	260	265	270	
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Glu Arg Leu Gln Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile	
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Tyr Val Leu Tyr Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu	
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Cys Thr Tyr Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu	
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Leu Phe Tyr His Val Ala Thr Asn Tyr Phe Pro Asn Leu Pro Gln Ala
 65 70 75 80

Leu Ser Asn Val Ala Trp Pro Leu Tyr Trp Ala Met Gln Gly Cys Ile
 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Leu His Ser
 115 120 125
 Ser Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Gly Leu Arg Trp Trp Ala Lys His Phe Asn Asn Pro Pro
 165 170 175
 Gly Arg Phe Leu Ser Ile Thr Ile Gln Leu Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ala Gly Arg Pro Tyr Asp Arg Phe Ala Cys
 195 200 205
 His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Asp Arg Glu Arg Leu Gln
 210 215 220
 Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Ala Tyr Ala Leu Tyr
 225 230 235 240
 Arg Leu Val Leu Ala Lys Gly Val Gly Trp Val Ile Ser Val Tyr Gly
 245 250 255
 Val Pro Leu Leu Val Val Asn Ala Phe Leu Val Met Ile Thr Tyr Leu
 260 265 270
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 275 280 285
 Trp Met Arg Gly Ala Leu Ser Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 305 310 315 320
 Phe Ser Thr Met Pro His Tyr His Ala Met Val Ala Thr Lys Ala Ile
 325 330 335
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Met Pro Val Tyr
 340 345 350
 Lys Ala Ile Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp
 355 360 365

Glu Gly Asp Lys Asp Lys Gly Val Phe Trp Phe Arg Asn Lys Leu
 370 375 380

<210> 7
 <211> 5006
 <212> DNA
 <213> Gossypium sp.

<220>
 <221> 5'UTR
 <222> (3785)..(5006)

<220>
 <221> intron
 <222> (3889)..(4998)

<400> 7
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 aaaggcccaa ctaatccaaa caaaacttga gtgttacaat ctaaccctag tctggcaacg 180
 gatacggggtt aagggtgtta caacctttac agtgatcaac gaacaaaacct tgagtggatt 240
 tggatttgac cccctaccc cactacacac aaggaagaat gttagtttag ttattcaata 300
 gctactaagt tgggtttacat atatatacaa gttccacact tgattctcaa tcaatgtgag 360
 actaatgctt ttcattttctc tcaacataat tcacaagtag cttactttga gtatcaattt 420
 ttcattcatc actcaatcat tttgagcata tgatatattg ttgtaaatgt ctaatggagt 480
 agaataataa attataattt tatgattcaa cttttcacct ttaccaatag aaaatatgcc 540
 tcaaagtttt caaaaaatca tttttttctc aatagaaata acttttagaca tcaagaatct 600
 acgaataaaa tttaaataac tttttttctc aatcttcgat acttgctatt aaattaactt 660
 aaattcttct acttgagatt ttgatgcatg cgacaaaaat tgagattaga atccatgatg 720
 tggaaagcaa aacaaatatg taagcaaata ttgtcttgtc gtaaaacat ttgatttttt 780
 ttttcaatca ttcattgaaa ttgaagtccc tcaatgaagc catcacataa tatgttacat 840
 aaaagttaga aacttaaacy tgatgatgca tgaacctctc taatttcact ctccaaaatt 900
 catcacgcaa gcgatacttc caatgaccca aaattattga aaccaatgtg cttttcctat 960
 cattgaaaat cgtgatggag ccacttgtaa cattgtttgc gtacatactt attattatta 1020

ttattattaa tattttattg ataaaagtat tagaaatfff tgtattaaaa gtcagattat 1080
 attttatatt ttaaaaataa ataagttagt cattctgtgt tagatcaa at agcaaaacaa 1140
 tagaaataga tgaaatfftc aataaaaaag gaccagttta ctctttgaac taacgcacaa 1200
 tgactaattt accattttta gtagatgagg taaaatataa tctagctcct tgtacagggg 1260
 ctccgtgat acttttacc ctttctatct cttctcaacg ataaataaaa atatgtttta 1320
 gaaaatfftg ttccaaaga taattacaaa gttaagtcaa acaagcagta acattgtttc 1380
 acttaatttc cctttcgaaa gaaaaactct tatttagaat aattgtcatt caaagtaact 1440
 atttttttta gaacagctat gcttggaaca atcatgttta gaacatggct ccattttaga 1500
 atatggttgt cgtttgagaa caactcctgc aaaggataac gaatgtttgg aacagtctct 1560
 atttagaata actgcgtttc aagaataatc atatttagaa caacctccat ttaaaacaat 1620
 agtggttttt tttaaaaga agagatatta ttcaaaatta gctctttcaa gaaaagcctc 1680
 accatagaac aactattatt aaaaataaag ctaaattcac aatttgccc ttgaagtata 1740
 ctcatTTTTT gactttggta tctaaacttt tctttgctc aatttgatac ctaaaatact 1800
 ctcaaattcc attttttgac agacattaaa aaaataatct tatagccaat cacaagcgc 1860
 cacgtggcgt ctttatgtaa aaagaaatat tttgtttaat taaatgtata tacacattaa 1920
 aaaataaaaa aatatagaac aacatataaa ttataaaca atctataaaa ataaaattta 1980
 caaaaatata ataattgaaa aaaaattagt tgaaattaat aatattatta aaaaatgtaa 2040
 aacatttgta aaaattataa aaaagtttta aaaataattt tctttataaa attctaaaat 2100
 atataattct aaaattgtaa aaaggatat aaatttcatt tttttcaatt actcgaaatt 2160
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 aaaatttata attatatatt tcaaaatttt ataaattttt ttatatgtta tatatgattt 2280
 ttacatttt taatcaatat aatataaaat actaaatttt tttaaaaaaa tgatacgtgg 2340
 catgtttctaa tatcgccaca tgaccggtga acgtcgggc aatggccagt caaagccaaa 2400
 agtatttttt taatatttaa ataattaatt ttatacttct atttttaatt ttaatttaat 2460
 atttttattt taaataaact taattgttat gtgatatttt ttcactgacc caaaacatgc 2520
 tatgtggagc ttttccatt agccaaagtt gccaaataga ttttttcaac gtgtgtttaca 2580

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 gacaattata ttgagaataa attaggttta gaacgggtca aaataattct tattcagtaa 2760
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 tgatggaaaa aaataaaaaa aattaaatth tagatgaata aagagtacat gggctataat 3000
 tagaattaac ctaaatttgt ttggttataa ctagaggttt tggttcaaag aattaatttc 3060
 taaatccgag tccaaccgc tttggatcag ccaaaggttc ttttaaatta ttttaattat 3120
 ttatatthaa attaaataat aaaatatata aatataatat aatttcacatc tttattgaat 3180
 cgagttaatc caaaattgaa gaatataaac tcaaactcga ctcaagatga atcgaaccgc 3240
 ttgactaaac tgaccaacc caacttgtht ttgagctaag tttgagthta atattthcaa 3300
 cttcacgttg gcttgacca gactgattaa ttattaaaca actaaaagaa ttttaataata 3360
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 gtgattatat gatttatgth taattthaaat gthtaattatt tatattthact tcaacaatag 3480
 tagtaacatt ctgtaatatg aatatgaatc cgatgattga gaagtgagag gtgttacata 3540
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 tgggagatat caaaaagagg cgggghaatg atgatgatga aagcgagaat catcagaatc 3660
 agaaaaaagg gaaaaggthg attaaagaaa agactctcat cctcactgat tctggtctth 3720
 cttcccaaca cgtagcatct aaccataacg cctcaaatcc gctgctctc tattthatttc 3780
 aaaaccactt gattaagthc cccctccgct ccataccact cgcccaaac caacacgcct 3840
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 thaatthctt tttttththc ththcatgth ththcatgth thgttgcatth aagtgataaa 3960
 thtgagthga tgatgththg tatatctct tagthaaactga cctththgaa atactagcat 4020
 ththththaat atcaagthga agaagaagaa gaattthgth atgcaaaagc thththaaagc 4080
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gaaagaagcc atgggtttcaa tttttgagag ttttaaattcc caaataccag agagcttcat 4200
 cgttttattca tatatatttta aacatttttt aaagcaagaa cttgtgattt gtttttaata 4260
 aaatatgcaa taaatttttta tatttttctgt aaatttaaaa ttttaatttt ctacttttaa 4320
 aatttaaaaa agtaaatttt aaaatatacc tttcattaaa tttaaattatt ataagtaatt 4380
 gagtattttt aatttttaaaa tttcacacat caaattaaaa aaaaagttaa cacttgcact 4440
 tgattttgaa aagtaaaagg attaaatttc aaattttcag taaaaggact aaatttcaaa 4500
 tttttaaaga gtatagagac tctctacat ttttagatttt aaaatttaaa tctaacagtt 4560
 aacactttct taattacttt acgataaatt taactaaaaa attacaatat taatgggttaa 4620
 aattaaattt tgaaaagtat aaagattaaa ttgtaaattt tcaaaaagca taggaagtta 4680
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<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
oligonucleotide useful as a primer

<400> 8

atggcktsa rgctbcatsc

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic

oligonucleotide useful as a primer

<400> 9
 tcasagyttn acytgyctat 20

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 10
 gcataggtca tggaccacgt 20

<210> 11
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 11
 gtaaaacgac ggccagt 17

<210> 12
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 12
 ggaaacagct atgaccatg 19

<210> 13
 <211> 8
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
oligonucleotide useful as a primer

<400> 13
ggcccggg

8

<210> 14
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide useful as a primer

<400> 14
ggcccccg

8

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide useful as a primer

<400> 15
ttttaatgcc atgcctcg

19

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide useful as a primer

<400> 16
cttcagcagt ccaagccctg

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 17
 cctggcggtta aactgctttc 20

<210> 18
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 18
 ccatatagtt tattaatata acac 24

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 19
 tatgttgcaa gtaggtgatc 20

<210> 20
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 20
 acgcgtcgac gtgtgttaca aaatggaccg aa 32

<210> 21
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 21
 cgcggatccg ctggctggac acgcaagaag ca 32

<210> 22
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 22
 cgagctcccc ctccgctcca taccact 27

<210> 23
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 23
 cgcggatccg ctggctttaa agaaagcagt t 31

<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 24
 catgtgacag atcgaaggaa 20

<210> 25
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide useful as a primer

<400> 25
 atctaattat tctattcaga c 21

<210> 26
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 peptide

<220>
 <221> UNSURE
 <222> (1)..(6)
 <223> Xaa at position 3 is either Trp or Cys

<400> 26
 His Glu Xaa Gly His His
 1 5

<210> 27
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 peptide

<400> 27
 His Arg Arg His His
 1 5

<210> 28
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 peptide

<400> 28

His Val Ala His His
1 5

<210> 29
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
peptide

<220>
<221> UNSURE
<222> (1)..(5)
<223> Xaa at position 2 is any amino acid; Xaa at
position 3 is any amino acid

<400> 29
His Xaa Xaa His His
1 5

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
peptide

<220>
<221> UNSURE
<222> (1)..(6)
<223> Xaa at position 2 is any amino acid; Xaa at
position 3 is any amino acid; Xaa at position 4 is
any amino acid

<400> 30
His Xaa Xaa Xaa His His
1 5

<210> 31
<211> 383
<212> PRT
<213> Glycine max

<400> 31

Met Gly Ala Gly Gly Arg Thr Asp Val Pro Pro Ala Asn Arg Lys Ser
 1 5 10 15
 Glu Val Asp Pro Leu Lys Arg Val Pro Phe Glu Lys Pro Gln Phe Ser
 20 25 30
 Leu Ser Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
 35 40 45
 Val Leu Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe
 50 55 60
 Cys Leu Tyr Tyr Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro
 65 70 75 80
 Leu Ser Phe Arg Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly Leu Ile Leu His Ser
 115 120 125
 Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Gln Lys Ser Cys Ile Lys Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro
 165 170 175
 Gly Arg Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
 195 200 205
 His Tyr Asp Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
 210 215 220
 Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Val Tyr Gly Leu Phe
 225 230 235 240
 Arg Leu Ala Met Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly
 245 250 255
 Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Phe Leu
 260 265 270

Gln His Thr His Pro Ala Leu Pro His Tyr Thr Ser Ser Glu Trp Asp
 275 280 285
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 305 310 315 320
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
 325 330 335
 Lys Pro Ile Leu Gly Glu Tyr Tyr Arg Phe Asp Glu Thr Pro Phe Val
 340 345 350
 Lys Ala Met Trp Arg Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro Asp
 355 360 365
 Gln Ser Thr Glu Ser Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 32
 <211> 383
 <212> PRT
 <213> Arabidopsis thaliana

<400> 32
 Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
 1 5 10 15
 Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
 20 25 30
 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65 70 75 80
 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125

Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	
130						135					140					
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
145					150					155					160	
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
				165					170					175		
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu	
			180					185					190			
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	
	195						200					205				
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln	
	210					215					220					
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr	
225					230					235					240	
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly	
				245					250					255		
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu	
			260					265					270			
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	
	275						280					285				
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	
	290					295					300					
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu	
305					310					315					320	
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile	
				325					330					335		
Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr	
		340						345					350			
Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp	
		355					360					365				
Arg	Glu	Gly	Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu		
	370					375					380					

<210> 33
<211> 387

<212> PRT

<213> Glycine max

<400> 33

Met	Gly	Leu	Ala	Lys	Glu	Thr	Thr	Met	Gly	Gly	Arg	Gly	Arg	Val	Ala	
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Lys	Val	Glu	Val	Gln	Gly	Lys	Lys	Pro	Leu	Ser	Arg	Val	Pro	Asn	Thr	
			20					25					30			
Lys	Pro	Pro	Phe	Thr	Val	Gly	Gln	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	
		35					40					45				
Cys	Phe	Gln	Arg	Ser	Leu	Leu	Thr	Ser	Phe	Ser	Tyr	Val	Val	Tyr	Asp	
	50					55					60					
Leu	Ser	Phe	Ala	Phe	Ile	Phe	Tyr	Ile	Ala	Thr	Thr	Tyr	Phe	His	Leu	
65					70					75					80	
Leu	Pro	Gln	Pro	Phe	Ser	Leu	Ile	Ala	Trp	Pro	Ile	Tyr	Trp	Val	Leu	
				85					90					95		
Gln	Gly	Cys	Leu	Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	
			100					105					110			
His	His	Ala	Phe	Ser	Lys	Tyr	Gln	Trp	Val	Asp	Asp	Val	Val	Gly	Leu	
		115					120					125				
Thr	Leu	His	Ser	Thr	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Ile	Ser	
	130					135						140				
His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Leu	Asp	Arg	Asp	Glu	Val	
145					150					155				160		
Phe	Val	Pro	Lys	Pro	Lys	Ser	Lys	Val	Ala	Trp	Phe	Ser	Lys	Tyr	Leu	
			165						170					175		
Asn	Asn	Pro	Leu	Gly	Arg	Ala	Val	Ser	Leu	Leu	Val	Thr	Leu	Thr	Ile	
			180					185					190			
Gly	Trp	Pro	Met	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	
		195				200						205				
Ser	Phe	Ala	Ser	His	Tyr	His	Pro	Tyr	Ala	Pro	Ile	Tyr	Ser	Asn	Arg	
	210					215					220					
Glu	Arg	Leu	Leu	Ile	Tyr	Val	Ser	Asp	Val	Ala	Leu	Phe	Ser	Val	Thr	
225					230					235				240		
Tyr	Ser	Leu	Tyr	Arg	Val	Ala	Thr	Leu	Lys	Gly	Leu	Val	Trp	Leu	Leu	
				245					250					255		

Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Thr
 260 265 270
 Ile Thr Tyr Leu Gln His Thr His Phe Ala Leu Pro His Tyr Asp Ser
 275 280 285
 Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr Met Asp Arg Asp
 290 295 300
 Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr Asp Thr His Val
 305 310 315 320
 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
 325 330 335
 Thr Asn Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp
 340 345 350
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr
 355 360 365
 Val Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg
 370 375 380
 Asn Lys Tyr
 385

<210> 34
 <211> 377
 <212> PRT
 <213> Brassica napus

<400> 34
 Met Val Val Ala Met Asp Gln Arg Ser Asn Ala Asn Gly Asp Glu Arg
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 Phe Asp Pro Ser Ala Gln Pro Pro Phe Lys Ile Gly Asp Ile Arg Ala
 20 25 30
 Ala Ile Pro Lys His Cys Trp Val Lys Ser Pro Leu Arg Ser Met Ser
 35 40 45
 Tyr Val Ala Arg Asp Ile Phe Ala Val Val Ala Leu Ala Val Ala Ala
 50 55 60
 Val Tyr Phe Asp Ser Trp Phe Phe Trp Pro Leu Tyr Trp Ala Ala Gln
 65 70 75 80
 Gly Thr Leu Phe Trp Ala Ile Phe Val Leu Gly His Asp Cys Gly His
 85 90 95

Gly Ser Phe Ser Asp Ile Pro Leu Leu Asn Thr Ala Val Gly His Ile
 100 105 110
 Leu His Ser Phe Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His
 115 120 125
 Arg Thr His His Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp
 130 135 140
 Val Pro Leu Pro Glu Lys Leu Tyr Lys Asn Leu Ser His Ser Thr Arg
 145 150 155 160
 Met Leu Arg Tyr Thr Val Pro Leu Pro Met Leu Ala Tyr Pro Leu Tyr
 165 170 175
 Leu Trp Tyr Arg Ser Pro Gly Lys Glu Gly Ser His Tyr Asn Pro Tyr
 180 185 190
 Ser Ser Leu Phe Ala Pro Ser Glu Arg Lys Leu Ile Ala Thr Ser Thr
 195 200 205
 Thr Cys Trp Ser Ile Met Leu Ala Thr Leu Val Tyr Leu Ser Phe Leu
 210 215 220
 Val Gly Pro Val Thr Val Leu Lys Val Tyr Gly Val Pro Tyr Ile Ile
 225 230 235 240
 Phe Val Met Trp Leu Asp Ala Val Thr Tyr Leu His His His Gly His
 245 250 255
 Asp Asp Lys Leu Pro Trp Tyr Arg Gly Lys Glu Trp Ser Tyr Leu Arg
 260 265 270
 Gly Gly Leu Thr Thr Ile Asp Arg Asp Tyr Gly Ile Phe Asn Asn Ile
 275 280 285
 His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln Ile
 290 295 300
 Pro His Tyr His Leu Val Asp Ala Thr Lys Ser Ala Lys His Val Leu
 305 310 315 320
 Gly Arg Tyr Tyr Arg Glu Pro Lys Thr Ser Gly Ala Ile Pro Ile His
 325 330 335
 Leu Val Glu Ser Leu Val Ala Ser Ile Lys Lys Asp His Tyr Val Ser
 340 345 350
 Asp Thr Gly Asp Ile Val Phe Tyr Glu Thr Asp Pro Asp Leu Tyr Val
 355 360 365

Tyr Ala Ser Asp Lys Ser Lys Ile Asn
 370 375

<210> 35
 <211> 424
 <212> PRT
 <213> Glycine max

<400> 35
 Met Ala Cys Thr Leu Ala Asp Ser Leu Leu Leu Phe Lys Gly Ser Tyr
 1 5 10 15

Gln Lys Pro Val Leu Arg Arg Asp Ile Ala Ala Arg Tyr Ser Pro Gly
 20 25 30

Ile Phe Ser Leu Asn Ser Asn Gly Leu Ile Gln Lys Arg Phe Arg Arg
 35 40 45

Gln Arg Asn Phe Val Thr Arg Asn Lys Val Thr Val Ile His Ala Val
 50 55 60

Ala Ile Pro Val Gln Pro Ala Pro Val Glu Ser Ala Glu Tyr Arg Lys
 65 70 75 80

Gln Leu Ala Glu Asp Tyr Gly Phe Arg Gln Val Gly Glu Pro Leu Ser
 85 90 95

Asp Asp Val Thr Leu Lys Asp Val Ile Asn Pro Leu Pro Lys Glu Val
 100 105 110

Phe Glu Ile Asp Asp Val Lys Ala Trp Lys Ser Val Leu Ile Ser Val
 115 120 125

Thr Ser Tyr Ala Leu Gly Leu Phe Met Ile Ser Lys Ala Pro Trp Tyr
 130 135 140

Leu Leu Pro Leu Ala Trp Val Trp Thr Gly Thr Ala Ile Thr Gly Phe
 145 150 155 160

Phe Val Ile Gly His Asp Cys Ala His Arg Ser Phe Ser Ser Asn Lys
 165 170 175

Leu Val Glu Asp Ile Val Gly Thr Leu Ala Phe Met Pro Leu Ile Tyr
 180 185 190

Pro Tyr Glu Pro Trp Arg Phe Lys His Asp Arg His His Ala Lys Thr
 195 200 205

Asn Met Leu Arg Glu Asp Thr Ala Trp His Pro Val Trp Lys Asp Glu
 210 215 220

Phe	Glu	Ser	Thr	Pro	Leu	Leu	Arg	Lys	Ala	Ile	Ile	Tyr	Gly	Tyr	Gly	225	230	235	240
Pro	Phe	Arg	Cys	Trp	Met	Ser	Ile	Ala	His	Trp	Leu	Met	Trp	His	Phe	245	250	255	
Asp	Leu	Lys	Lys	Phe	Arg	Pro	Ser	Glu	Val	Pro	Arg	Val	Lys	Ile	Ser	260	265	270	
Leu	Ala	Cys	Val	Phe	Ala	Phe	Ile	Ala	Ile	Gly	Trp	Pro	Leu	Ile	Ile	275	280	285	
Tyr	Lys	Thr	Gly	Ile	Met	Gly	Trp	Ile	Lys	Phe	Trp	Leu	Met	Pro	Trp	290	295	300	
Leu	Gly	Tyr	His	Phe	Trp	Met	Ser	Thr	Phe	Thr	Met	Val	His	His	Thr	305	310	315	320
Ala	Pro	Tyr	Ile	Pro	Phe	Lys	Tyr	Ser	Glu	Glu	Trp	Asn	Arg	Ala	Gln	325	330	335	
Ala	Gln	Leu	Asn	Gly	Thr	Val	His	Cys	Asp	Tyr	Pro	Lys	Trp	Ile	Glu	340	345	350	
Ile	Leu	Cys	His	Asp	Ile	Asn	Val	His	Ile	Pro	His	His	Ile	Ser	Pro	355	360	365	
Arg	Ile	Pro	Ser	Tyr	Asn	Leu	Arg	Ala	Ala	His	Lys	Ser	Leu	Gln	Glu	370	375	380	
Asn	Trp	Gly	Gln	Tyr	Leu	Asn	Glu	Ala	Ser	Trp	Asn	Trp	Arg	Leu	Met	385	390	395	400
Lys	Thr	Ile	Met	Thr	Val	Cys	Gln	Val	Tyr	Asp	Lys	Glu	Lys	Ser	Leu	405	410	415	
Cys	Cys	Leu	Arg	Arg	Thr	Cys	Pro	420											